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LOCUS	SCC77	33801 bp	DNA	BCT	10-MAY-2000
DEFINITION	Streptomyces coelicolor cosmid C77.				
ACCESSION	AL136503				
VERSION	AL136503.1 GI:6714747				
KEYWORDS	adenosine deaminase; carbohydrate kinase; dehydratase; dihydrodipicolinate synthase; DNA-binding protein; DnaJ protein; dnaJ2; Era-like GTP-binding protein; GTP-binding protein; heat-inducible transcriptional repressor; Hit-family protein; hrcA; hydrolase; IclR-family transcriptional regulator; lepA; lipoprotein; long-chain fatty-acid CoA ligase; oxidoreductase; oxygen-independent coproporphyrinogen III oxidase; protease; transmembrane efflux protein; transmembrane transport protein.				
SOURCE	Streptomyces coelicolor A3(2).				
ORGANISM	Streptomyces coelicolor A3(2) Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.				
REFERENCE	1 (bases 1 to 33801)				
AUTHORS	Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J., Kinashi,H. and Hopwood,D.A.				
TITLE	A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome				
JOURNAL	Mol. Microbiol. 21 (1), 77-96 (1996)				
MEDLINE	97000351				
REFERENCE	2 (bases 1 to 33801)				
AUTHORS	Oliver,K. and Harris,D.				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 33801)				
AUTHORS	Thomson,N.R., Parkhill,J., Barrell,B.G. and Rajandream,M.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-JAN-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK				

alignment scores:

Quality:	397.00	Length:	363
Ratio:	1.829	Gaps:	10
Percent Similarity:	59.780	Percent Identity:	33.609

alignment block:

US-09-477-962-115 x SCC77/rev ..

Align seq 1/1 to reverse of: SCC77 from: 1 to: 33801

```

      11 IleProAlaIleArgGluAlaLeuGlyAspGluLysAspProArgLeuAl 27
          ::|||  ::|||::  ||  ||::
26678 CTGCCCGCG.....TCCGCGCTCGCCGGGGCCGCCGACCGCCCCCTCGG 26635

```

[illegible]

44 rpValThrAspIleProValAlaArgLeuArgGlyAspSer..... 57
:: ||| :::::::::::||||||| ::
26584 TCAACAGC::TACACCGCCACCGAACTGCGCGGCACCGGCGGGGTGCTC 26538

58	ArgGluArgSerProTyrValThrAlaLeuCysAspGlnIleArgPheTy	74
	::: ::: ::: :: ::: :	
26537	GCCTCCCGCACAACACTACGCCGACACCCTCGTCGACGAGGTCCGC.....	26493
74	rGlyProGlnLeuThrArg.....LeuGlyTyrArgPro.....G	86
	::: :::	:
26492CTGGCCCCGAAGGTGCTCGGCGACGACCCCCGCGAGGTCC	26453
86	luValMetTyrTrpGlyGlyGlyThrProThrArgLeuThrGlyAspGlu	102
	:~::~: ::: :	
26452	GCACGGTCTTCGTCGCGCGGCGGTACGCCCACCCTGCTGGCCCGCGGCGAC	26403
103	MetThrAlaValHisGlnAlaLeuAspAspAlaPheAspLeuThrGlyLe	119
	:~::~: ::: :::	
26402	CTGGTGCGGATGCTGGGCGCGATCCGCGACGAGTTCGGCCTGGCACCGGA	26353
119	uArgGlnTrpSerValGluSerThrProAsnAspLeuAspProAlaThrL	136
	::: ~:::: ~:::: ~:::: ~:::: ~::::	
26352	CGCGGAGATCACCAACGAGGCCAACCCGGAGTCCGTCGACCCGGCGTATC	26303
136	euAspThrLeuArgGlyLeuGlyValThrArgValSerValGlyValGln	152
	~:::: ::: ~:::: :::	
26302	TCGCCACCCTCCGCGCGGGCGGCTTCAACCGGATCTCCTTCGGCATGCAG	26253
153	SerLeuAsnProTyrGlnLeuArgLysAlaGlyArgAlaHisSerArgGl	169
	::: ::: ~::~: ~:::: ~::~:	
26252	AGCGCCAAGCAGCACGTCTGAAGATCCTGGACCGCACCCACACCCCGGG	26203
169	uGlnAlaLeuAlaAlaValProLeuLeuArgArgAlaGlyIleAspGluP	186
	::: ~:::: ~:::: ~::~:	
26202	ACGCCCCGAGGCCTGTGTGCGCGAGGCCCGCGCGGCCGGCTTCGACCACG	26153
186	heAsnValAspLeuIleAlaGlyPheProGlyGluAlaValGluSerPhe	202
	~:::: ~:::: ~:::: ~::~:	
26152	TCAACCTCGACCTGATCTACGGCACCCCGGCGAGTCCGACGACGACTGG	26103
203	GluGluThrLeuArgThrValLeuAlaLeuAspProProHisValSerVa	219
	::: ~: ~:::: ~::~: ~:::: ~::~:	
26102	CGGGCCTCCCTGGACGCCGCGCTCGGCGCCGACCCGACCACGTCTCGGC	26053
219	lTyrProTyrArgAlaThrProLysThrValMetAlaMetGlnLeuAspA	236
	: ~: ~: ~::~:	
26052	GTACGCCCTGATCGTCGAGGAGGGCACCCAGCTCGCCCGCCGCATCCGC	26003
236	rgGluPheValGluAlaArgAsnArgAspGlyMetIleAspAlaTyrGlu	252
	:::	
26002	GCGGCGAGGTCCCGATGACCGACGACGACGTGCACGCCGACCGGTACCTG	25953
253	ArgAlaMetAlaAlaLeuGlyAlaAlaGlyTyrHisGluTyrCysHisGl	269
	~:::: ~:::: ~:::: ~::::	::
25952	ATCGCCGAGGAGGCACTGTCCGCGGCCGGTTACGACTGGTACGAGGTGTC	25903
269	yTyrTrpValArgAsp.....AlaArgHisGluAspGlnAspG	282
	: ~::~: ::: ~:	
25902	CAACTGGGCCACCTCCGACGCGGGGCGCTGCCTGCAC.....	25866

282 lyAsnTyrLysTyrAspLeuAlaGlyAspLysIleGlyPheGlySerGly 298
 ||| ||| ::::: ||| ||| |||
 25865 ..AACGAGCTGTACTGGCGGGGCGCCGACTGGTGGGGCGCCGGACCGGGC 25818

 299 AlaGluSerIleIleGlyHisHisLeuLeuTrpAsn.....GluAsnSe 313
 |||::: ||| ::: ||| ||||| ::: ::
 25817 GCGCACTCCCACGTGGGGGGCGTGCGGTGGTGGAACTGAAGCACCCGGG 25768

 313 rAlaTyrAlaArgTyrLeuLeuAlaProArgGluPheSerAlaAlaHisA 330
 :||||||| ||| ||| ::::: :::|||: :::::
 25767 GCGGTACGCGGGGGCGCTGGCGGGCGGGCAAGTCGCCGGGCGCGGGGCGCG 25718

 330 rgPheThrThrAlaGluProAspArgLeuThrAlaProValGlyGlyAla 346
 ::::: ||| ||| ||||| ::: :::
 25717 AGATCCTCACGGACGAG...GACCGGCGCGTGGAGCGCATCCTGCTGGAG 25671

 347 LeuMetThrArgGluGlyValValPheAlaArgPheArg 359
 ||| ||||| ||||| ::::: :::|||
 25670 CTGCGCCTGCGGGAGGGCGTCCCGCTGTCGCTGCTGCGG 25632

NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Books

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☐ 1: AL136503. Streptomyces coel...[gi:6714747]

Related Sequences, Protein, PubMed, Taxonomy

LOCUS SCC77 33801 bp DNA linear BCT 10-MAY-2000

DEFINITION Streptomyces coelicolor cosmid C77.

ACCESSION AL136503

VERSION AL136503.1 GI:6714747

KEYWORDS adenosine deaminase; carbohydrate kinase; dehydratase; dihydrodipicolinate synthase; DNA-binding protein; DnaJ protein; dnaJ2; Era-like GTP-binding protein; GTP-binding protein; heat-inducible transcriptional repressor; Hit-family protein; hrcA; hydrolase; IclR-family transcriptional regulator; lepA; lipoprotein; long-chain fatty-acid CoA ligase; oxidoreductase; oxygen-independent coproporphyrinogen III oxidase; protease; transmembrane efflux protein; transmembrane transport protein.

SOURCE Streptomyces coelicolor A3(2).

ORGANISM Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

REFERENCE 1 (bases 1 to 33801)

AUTHORS Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J., Kinashi,H. and Hopwood,D.A.

TITLE A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome

JOURNAL Mol. Microbiol. 21 (1), 77-96 (1996)

MEDLINE 97000351

REFERENCE 2 (bases 1 to 33801)

AUTHORS Oliver,K. and Harris,D.

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 33801)

AUTHORS Thomson,N.R., Parkhill,J., Barrell,B.G. and Rajandream,M.A.

TITLE Direct Submission

JOURNAL Submitted (17-JAN-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK

COMMENT Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary strand).
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
Gene prediction is based on positional base preference in codons



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	Books
Search	Nucleotide	▼ for					Go	Clear
		Limits	Preview/Index	History	Clipboard		Details	
Display	default	▼	Save	Text	Add to Clipboard			

☐ 1: CAB66237. putative oxygen-i...[gi:6714773]

Nucleotide, Related Sequences, PubMed, Taxonomy,
BLink, LinkOut

LOCUS CAB66237 435 aa linear BCT 10-MAY-2000
 DEFINITION putative oxygen-independent coproporphyrinogen III oxidase.
 [Streptomyces coelicolor A3(2)].
 ACCESSION CAB66237
 PID g6714773
 VERSION CAB66237.1 GI:6714773
 DBSOURCE embi locus SCC77, accession AL136503.1
 KEYWORDS .
 SOURCE Streptomyces coelicolor A3(2).
 ORGANISM Streptomyces coelicolor A3(2)
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 REFERENCE 1 (residues 1 to 435)
 AUTHORS Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
 Kinashi, H. and Hopwood, D.A.
 TITLE A set of ordered cosmids and a detailed genetic and physical map
 for the 8 Mb Streptomyces coelicolor A3(2) chromosome
 JOURNAL Mol. Microbiol. 21 (1), 77-96 (1996)
 MEDLINE 97000351
 REFERENCE 2 (residues 1 to 435)
 AUTHORS Oliver, K. and Harris, D.
 JOURNAL Unpublished
 REFERENCE 3 (residues 1 to 435)
 AUTHORS Thomson, N.R., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
 TITLE Direct Submission
 JOURNAL Submitted (17-JAN-2000) Streptomyces coelicolor sequencing project,
 Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
 CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
 David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
 Colney, Norwich, Norfolk NR4 7UH, UK
 COMMENT Notes:
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 Details of S. coelicolor sequencing at the Sanger Centre are
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 (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
 CDS are numbered using the following system eg SC7B7.01c. SC (S.
 coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
 strand).
 The more significant matches with motifs in the PROSITE database
 are also included but some of these may be fortuitous.
 The length in codons is given for each CDS.
 Usually, the highest scoring match found by fasta -o is given for
 CDS which show significant similarity to other CDS in the database.
 The position of possible ribosome binding site sequences are given
 where these have been used to deduce the initiation codon.
 Gene prediction is based on positional base preference in codons
 using a specially developed Hidden Markov Model (Krogh et al.,
 Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot
 program of Bibb et al., Gene 30:157-66(1984) as implemented at

<http://www.nih.gov/jun/cgi-bin/frameplot.pl>. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid C77 Lies between and overlaps with cosmids C117 and C123 on the AseI-C genomic restriction fragment.

FEATURES	Location/Qualifiers
source	1..435 /organism="Streptomyces coelicolor A3(2)" /strain="A3(2)" /db_xref="taxon:100226" /clone="cosmid C77"
Protein	1..435 /product="putative oxygen-independent coproporphyrinogen III oxidase."
CDS	1..435 /gene="SCC77.26c" /coded_by="complement(AL136503.1:25494..26801)" /transl_table=11 /note="SCC77.26c, possible oxygen-independent coproporphyrinogen III oxidase (EC 1.-.-.-), len: 435 aa. Highly similar to many putative coproporphyrinogen III oxidases including: Bacillus subtilis SW:HEMN_BACSU(EMBL:X91655) probable oxygen-independent coproporphyrinogen III oxidase (366 aa), fasta scores opt: 490 z-score: 555.3 E(): 1.5e-23 30.8% identity in 328 aa overlap and Mycobacterium tuberculosis SW:HEMN_MYCTU(EMBL:Z81368) probable oxygen-independent coproporphyrinogen III oxidase (375 aa), fasta scores opt: 1358 z-score: 1530.5 E(): 0 56.5% identity in 382 aa overlap. Contains a Prosite hit to PS00017 ATP/GTP-binding site motif A (P-loop)."

ORIGIN

```
1 mngrrreraagg tewagdpagc gtmermpsal pdgepvpadg alpasalaga adrplgfyh  
61 vpycatrcgy cdfntytate lrgtggvlas rdnyadtlvd evrlarkvlg ddpvrvrtvf  
121 vgggtptlla agdlvrmlga irdefglapd aeitteanpe svdpaylatl raggfnrisf  
181 gmqsakqhvl kildrthtpg rpeacvaear aagfdhvnld liygtpgesd ddwraslada  
241 lgagpdhvsa yaliveegtq larrirrgew pmtdddvhad ryliaeeals aagydwyevs  
301 nwatsdagrc lhnelywrga dwwgagpgah shvggvrwnn vkhpGayaga laagkspgag  
361 reiltdedrr verillelrl regvplsllr eaglaasrra lsegllqegp yeagsavltl  
421 rgrlladavv rdlvd
```

//

Revised: October 24, 2001.

Disclaimer: Write to the Help Desk

NCBI NLM NIH

alignment_block:
us-09-477-962-115 x US-09-477-962-1 ..

Align seg 1/1 to: US-09-477-962-1 from: 1 to: 58857

Seg 1 = 58857 bp
57,583-58,854

= 1271 bp

1 MetSerHisAlaIleGlyProSerArgLeuIleProAlaIleArgGluAl 17
|||||
57583 ATGAGCCACGCCATCGGACCGAGCCGGCTGATCCCCGCCATCCGCGAAGC 57632
Seg 5
17 aLeuGlyAspGluLysAspProArgLeuAlaLeuTyrValHisValProP 34
|||||
57633 GCTCGGGGACGAGAAGGACCCCCGGCTCGCCCTCTACGTCCACGTCCCCT 57682
34 heCysSerSerLysCysHisPheCysAspTrpValThrAspIleProVal 50
|||||
57683 TCTGCTCCTCCAAGTGCCACTTCTGCGACTGGGTACCGACATCCCCGTC 57732
51 AlaArgLeuArgGlyAspSerArgGluArgSerProTyrValThrAlaLe 67
|||||
57733 GCACGCCTGCGCGGCGACAGCCGGGAACGCTCGCCCTACGTCACCGCCCT 57782
67 uCysAspGlnIleArgPheTyrGlyProGlnLeuThrArgLeuGlyTyrA 84
|||||
57783 CTGCGACCAGATCCGCTTCTACGGCCCCAGCTACCCGGCTCGGCTACC 57832
84 rgProGluValMetTyrTrpGlyGlyGlyThrProThrArgLeuThrGly 100
|||||
57833 GCCCCGAGGTCATGTACTGGGGCGGCGGCACCCCCACCCGGCTCACCGGC 57882
101 AspGluMetThrAlaValHisGlnAlaLeuAspAspAlaPheAspLeuTh 117
|||||
57883 GACGAGATGACGGCCGTCCACCAGGCCCTCGACGACGCCTTCGACCTGAC 57932
117 rGlyLeuArgGlnTrpSerValGluSerThrProAsnAspLeuAspProA 134
|||||
57933 GGGACTCCGCCAGTGGTCGGTGGAGAGCACCCCGAACGACCTCGACCCCG 57982
134 laThrLeuAspThrLeuArgGlyLeuGlyValThrArgValSerValGly 150
|||||
57983 CCACCCTCGACACCCTGCGGGCCTCGGCGTCACCCGCGTCAGCGTCGGC 58032
151 ValGlnSerLeuAsnProTyrGlnLeuArgLysAlaGlyArgAlaHisSe 167
|||||
58033 GTCCAGTCGCTCAACCCGTACCAGCTGCGCAAGGCAGGCCGGGCCACTC 58082
167 rArgGluGlnAlaLeuAlaAlaValProLeuLeuArgArgAlaGlyIleA 184
|||||
58083 GCGCGAACAGGCCCTGGCCGCCGTCCCCCTGTTGCGCCGCGCCGGCATCG 58132
184 spGluPheAsnValAspLeuIleAlaGlyPheProGlyGluAlaValGlu 200
|||||
58133 ACCAGTTCACCGTCCACCTGATCGCCGGCTTCCCCGGCGAAGCCGTCGAG 58182
201 SerPheGluGluThrLeuArgThrValLeuAlaLeuAspProProHisVa 217
|||||
58183 TCCTTCGAGGAGACCCTGGCACCCTCCTCGGCTCGACCGCGCGCACGT 58232

217 lSerValTyrProTyrArgAlaThrProLysThrValMetAlaMetGlnL 234
 |||||
 58233 CTCCGTCTACCCCTACCGCGCCACCCCAAGACGGTCATGGCCATGCAGC 58282

 234 euAspArgGluPheValGluAlaArgAsnArgAspGlyMetIleAspAla 250
 |||||
 58283 TCGACCGCGAGTTCGTCTGAGGCCCGGAACCGGGACGGCATGATCGACGCC 58332

 251 TyrGluArgAlaMetAlaAlaLeuGlyAlaAlaGlyTyrHisGluTyrCy 267
 |||||
 58333 TATGAACGGGCCATGGCCGCGCTCGGCGCCGCCGGCTATCACGAGTACTG 58382

 267 sHisGlyTyrTrpValArgAspAlaArgHisGluAspGlnAspGlyAsnT 284
 |||||
 58383 CCACGGCTACTGGGTGCGCGACGCGCGCCACGAGGACCAGGACGGCAACT 58432

 284 yrLysTyrAspLeuAlaGlyAspLysIleGlyPheGlySerGlyAlaGlu 300
 |||||
 58433 ACAAGTACGACCTGGCCGGCGACAAGATCGGCTTTGGCAGCGGCGCCGAA 58482

 301 SerIleIleGlyHisHisLeuLeuTrpAsnGluAsnSerAlaTyrAlaAr 317
 |||||
 58483 TCGATCATCGGTACACACCTGCTCTGGAACGAGAACAGCGCCTACGCCCG 58532

 317 gTyrLeuLeuAlaProArgGluPheSerAlaAlaHisArgPheThrThrA 334
 |||||
 58533 CTACCTGCTCGCCCCCGCGAGTTCTCCGCCGCCACCGGTTACACCACG 58582

 334 laGluProAspArgLeuThrAlaProValGlyGlyAlaLeuMetThrArg 350
 |||||
 58583 CCGAACCCGACCGCCTGACCGCCCCCGTCGGCGGCGCGCTGATGACCCGT 58632

 351 GluGlyValValPheAlaArgPheArgArgLeuThrGlyLeuAspPheAl 367
 |||||
 58633 GAAGGCGTGGTCTTCGCCCCTTCCGCAGACTGACCGGCCTGGACTTCGC 58682

 367 aAspValArgAlaThrProTyrPheArgGlnTrpPheGluLeuLeuGluA 384
 |||||
 58683 GGACGTCCGCGCCACACCGTACTTCCGCCAGTGTTTCGAGCTCCTGGAGC 58732

 384 rgCysGlyGlyArgPheValGluThrProTyrSerLeuArgLeuGluPro 400
 |||||
 58733 GCTGCGGCGGCCGCTTCGTCTGAGACGCCGTACAGCCTCCGCCTGGAGCCG 58782

 401 SerThrIleHisArgAlaTyrIleThrHisLeuAlaTyrThrMetAlaHi 417
 |||||
 58783 TCCACCATCCACCGCGCCTACATCACCCACCTCGCCTACACCATGGCCCA 58832

 417 sGlyLeuAlaProGluArgAla 424
 |||||
 58833 TGGCCTGGCCCCCGAACGCGCC 58854

L1 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS
AN 2000:332950 CAPLUS
TI Bleomycin biosynthesis in Streptomyces verticillus ATCC15003: A model for
hybrid peptide and polyketide biosynthesis.
AU Du, Liangcheng; Sanchez, Cesar; Chen, Mei; Edwards, Daniel J.; Murrell,
Jeffrey M.; Shen, Ben
CS Department of Chemistry, University of California, Davis, CA, 95616, USA
SO Book of Abstracts, 219th ACS National Meeting, San Francisco, CA, March
26-30, 2000 (2000), ORGN-822 Publisher: American Chemical Society,
Washington, D. C.
CODEN: 69CLAC
DT Conference; Meeting Abstract
LA English

=> d abs

L1 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS
AB Polyketides and nonribosomal peptides are assembled in a remarkably
similar fashion by polyketide synthases (PKSs) from short carboxylic acids
and nonribosomal peptide synthetases (NRPSs) from amino acids, resp.
Cloning and sequence anal. of the 90-kb bleomycin (BLM) biosynthesis
cluster from Streptomyces verticillus ATCC15003 revealed both NRPS and PKS
genes. By detg. the substrate specificity of individual NRPS and PKS
modules, a linear hybrid NRPS/PKS/NRPS model is formulated for the Blm
megasyntetase-templated assembly of BLM from nine amino acids and one
acetate. These results set the stage for engineering novel BLM analogs by
genetic manipulation of the blm biosynthesis genes, support the wisdom of
combining individual NRPS and PKS modules for combinatorial biosynthesis,
and lay the foundation to investigate the mol. basis for intermodular
communication between NRPS and PKS and the mechanism for bithiazole
biosynthesis.

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L3 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS
AN 1999:145586 CAPLUS
TI Bleomycin biosynthesis in streptomyces verticillus ATCC15003: The search
for a hybrid polyketide and peptide biosynthetic system
AU Shen, Ben; Du, Liangcheng; Edwards, Dan; Chen, Mei; Sanchez, Cesar
CS Department of Chemistry, University of California, Davis, CA, 95616, USA
SO Book of Abstracts, 217th ACS National Meeting, Anaheim, Calif., March
21-25 (1999), ORGN-153 Publisher: American Chemical Society, Washington,
D. C.
CODEN: 67GHA6
DT Conference; Meeting Abstract
LA English

=> d abs

L3 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS
AB The biosynthesis of bleomycin (Blm) in Sv. ATCC15003 has been studied as a
model to decipher the mechanism of how peptide synthase (PTS) and
polyketide synthase (PKS) can be hybridized into a functional system to
make metabolite from amino acids and short fatty acids. A 110kb gene
cluster for Blm biosynthesis was cloned from Sv. ATCC15003, 75kb of which
has been fully sequenced and analyzed. Among the many novel discoveries
made from this study are:. (1) the first model for a hybrid PTS/PKS/PTS
biosynthetic system, (2) the first example of PKS gene from actinomycetes
that contains a MT domain, and (3) a novel mechanism for bithiazole
biosynthesis. These results should lay the foundation for rational
engineering of hybrid PTS/PKS biosynthetic systems from other peptide and
polyketide biosynthetic pathways to generate structural diversity.

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